SEQUENCE LISTING

<110> Sumitomo Chemical Co., Ltd.

<120> ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY TO CYTOKININ RECEPTOR

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<170> PatentIn Ver. 2.1

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Tyr Leu Gly Gly Val Phe Asp Ile Glu Ser Leu Val Glu Asn Leu Leu
325 330 335

caa cag ctg gct agc aag caa acg att ctt gtc aat gtg tac gat atc 1056

Gln Gln Leu Ala Ser Lys Gln Thr Ile Leu Val Asn Val Tyr Asp Ile
340 345 350

acc aat cac tct caa ccg att agc atg tat ggt aca aat gtg tcg gct 1104

Thr Asn His Ser Gln Pro Ile Ser Met Tyr Gly Thr Asn Val Ser Ala
355 360 365

gat ggg ttg gaa cgt gtt agt cca cta atc ttt ggc gat cca ttg aga 1152

Asp Gly Leu Glu Arg Val Ser Pro Leu Ile Phe Gly Asp Pro Leu Arg
370 375 380

aag cat gag atg cgt tgc aga ttt aag cag aaa cca cca tgg cca gtg 1200

Lys His Glu Met Arg Cys Arg Phe Lys Gln Lys Pro Pro Trp Pro Val
385 390 395 400

cta tca atg gtg aca tca ttc ggt atc ctt gtg att gcg tta ctt gtt 1248

Leu Ser Met Val Thr Ser Phe Gly Ile Leu Val Ile Ala Leu Leu Val
405 410 415

gca cat ata atc cac gca acc gtt agt cga ata cac aaa gtt gaa gaa 1296

Ala His Ile Ile His Ala Thr Val Ser Arg Ile His Lys Val Glu Glu
420 425 430

gat tgt gat aaa atg aag cag ctc aag aaa aag gct gaa gca gca gat 1344

Asp Cys Asp Lys Met Lys Gln Leu Lys Lys Lys Ala Glu Ala Ala Asp
435 440 445

gtt gca aag tca cag ttc ctt gcc act gtt tca cat gaa atc aga act 1392

Val Ala Lys Ser Gln Phe Leu Ala Thr Val Ser His Glu Ile Arg Thr
450 455 460

cca atg aat ggt gtt cta gga atg ttg cat atg ctt atg gac aca gag 1440

Pro Met Asn Gly Val Leu Gly Met Leu His Met Leu Met Asp Thr Glu
465 470 475 480

tta gat gtt acg caa cag gat tat gtt agg acc gca cag gca agt gga 1488

Leu Asp Val Thr Gln Gln Asp Tyr Val Arg Thr Ala Gln Ala Ser Gly
485 490 495

aaa gct tta gtc tcg cta ata aat gag gtt ttg gac caa gca aag att 1536

Lys Ala Leu Val Ser Leu Ile Asn Glu Val Leu Asp Gln Ala Lys Ile
500 505 510

gaa tct gga aag ctt gaa ctt gag gag gtg cgg ttt gat ttg aga gga 1584

Glu Ser Gly Lys Leu Glu Leu Glu Glu Val Arg Phe Asp Leu Arg Gly
515 520 525

ata tta gat gat gtc ctg tca ctc ttc tct agc aag tcc caa caa aag 1632

Ile Leu Asp Asp Val Leu Ser Leu Phe Ser Ser Lys Ser Gln Gln Lys
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Gly Val Glu Leu Ala Val Tyr Ile Ser Asp Arg Val Pro Asp Met Leu
545 550 555 560

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Ile Gly Asp Pro Gly Arg Phe Arg Gln Ile Leu Thr Asn Leu Met Gly
565 570 575

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Asn Ser Ile Lys Phe Thr Glu Lys Gly His Ile Phe Val Thr Val His
580 585 590

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Leu Val Asp Glu Leu Phe Glu Ser Ile Asp Gly Glu Thr Ala Ser Ser
595 600 605

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Pro Glu Ser Thr Leu Ser Gly Leu Pro Val Ala Asp Arg Gln Arg Ser

610 615 620

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Trp Glu Asn Phe Lys Ala Phe Ser Ser Asn Gly His Arg Ser Phe Glu
625 630 635 640

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Pro Ser Pro Pro Asp Ile Asn Leu Ile Val Ser Val Glu Asp Thr Gly
645 650 655

gta ggg atc cct gta gaa gcg cag tcc cgt att ttt acg cct ttc atg 2016

Val Gly Ile Pro Val Glu Ala Gln Ser Arg Ile Phe Thr Pro Phe Met
660 665 670

caa gtc gga cca tcc ata tcc agg acg cat gga ggc aca gga att gga 2064

Gln Val Gly Pro Ser Ile Ser Arg Thr His Gly Gly Thr Gly Ile Gly
675 680 685

ctt agc ata agc aaa tgt cta gtt gga ctg atg aag gga gaa att gga 2112

Leu Ser Ile Ser Lys Cys Leu Val Gly Leu Met Lys Gly Glu Ile Gly
690 695 700

ttc tcg agt act ccc aag gtt ggg tcc aca ttc aca ttt act gct gta 2160

Phe Ser Ser Thr Pro Lys Val Gly Ser Thr Phe Thr Phe Thr Ala Val
705 710 715 720

ttt tcc aat ggg atg caa cca gct gaa aga aag aat gac aac aac cag 2208

Phe Ser Asn Gly Met Gln Pro Ala Glu Arg Lys Asn Asp Asn Asn Gln
725 730 735

ccc ata ttc tcg gaa ttc cgg ggc atg aaa gct gtg gtt gtg gac cat 2256

Pro Ile Phe Ser Glu Phe Arg Gly Met Lys Ala Val Val Val Asp His
740 745 750

agg cct gca agg gca aaa gtc tcg tgg tac cat ttt cag cgt ctt gga 2304

Arg Pro Ala Arg Ala Lys Val Ser Trp Tyr His Phe Gln Arg Leu Gly
755 760 765

att cga gtc gaa gta gtt cca cgt gtt gaa cag gct cta cat tat ctg 2352

Ile Arg Val Glu Val Val Pro Arg Val Glu Gln Ala Leu His Tyr Leu
770 775 780

aag att ggt act acc act gtg aat atg ata ctc ata gag caa gaa ata 2400

Lys Ile Gly Thr Thr Thr Val Asn Met Ile Leu Ile Glu Gln Glu Ile
785 790 795 800

tgg aat agg gaa gca gat gat ttc att aaa aag cta cag aaa gac cct 2448

Trp Asn Arg Glu Ala Asp Asp Phe Ile Lys Lys Leu Gln Lys Asp Pro
805 810 815

ctt ttc ctt tct cct aag ttg att ttg tta gca aac tca gta gaa tcg 2496

Leu Phe Leu Ser Pro Lys Leu Ile Leu Leu Ala Asn Ser Val Glu Ser
820 825 830

tca ata tca gag gct tta tgc acc ggt ata gat cct cca ata gtg ata 2544

Ser Ile Ser Glu Ala Leu Cys Thr Gly Ile Asp Pro Pro Ile Val Ile
835 840 845

gtg aaa cca ttg agg gcg agt atg cta gca gca act ttg cag agg gga 2592

Val Lys Pro Leu Arg Ala Ser Met Leu Ala Ala Thr Leu Gln Arg Gly
850 855 860

ttg ggt att gga atc aga gaa cca cct caa cac aag gga cct cct gct 2640

Leu Gly Ile Gly Ile Arg Glu Pro Pro Gln His Lys Gly Pro Pro Ala
865 870 875 880

ttg att ctc agg aat ctt ctc ctt ggt aga aaa att tta atc gtg gat 2688

Leu Ile Leu Arg Asn Leu Leu Leu Gly Arg Lys Ile Leu Ile Val Asp
885 890 895

gat aac aac gta aac ctc aga gtg gca gcg gga gct ctg aaa aag tac 2736

Asp Asn Asn Val Asn Leu Arg Val Ala Ala Gly Ala Leu Lys Lys Tyr
900 905 910

gga gct gat gtg gtc tgc gct gag agt ggg ata aag gca atc tca ttg 2784

Gly Ala Asp Val Val Cys Ala Glu Ser Gly Ile Lys Ala Ile Ser Leu
915 920 925

ctt aag cca cct cac gag ttt gat gct tgc ttc atg gac att cag atg 2832

Leu Lys Pro Pro His Glu Phe Asp Ala Cys Phe Met Asp Ile Gln Met
930 935 940

cca gaa atg gat gga ttt gaa gct aca agg aga ata cga gat atg gaa 2880

Pro Glu Met Asp Gly Phe Glu Ala Thr Arg Arg Ile Arg Asp Met Glu
945 950 955 960

gag gag atg aac aag aga ata aag aat ggg gag gct ttg ata gta gag 2928

Glu Glu Met Asn Lys Arg Ile Lys Asn Gly Glu Ala Leu Ile Val Glu
965 970 975

aac ggt aac aaa aca agc tgg cat ctt ccg gta tta gca atg acg gca 2976

Asn Gly Asn Lys Thr Ser Trp His Leu Pro Val Leu Ala Met Thr Ala
980 985 990

gat gtg atc caa gca acg cat gag gaa tgt ctg aag tgt gga atg gat 3024

Asp Val Ile Gln Ala Thr His Glu Glu Cys Leu Lys Cys Gly Met Asp
995 1000 1005

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Gly Tyr Val Ser Lys Pro Phe Glu Ala Glu Gln Leu Tyr Arg Glu Val
1010 1015 1020

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Ile Glu Asp Lys Ser Gly Leu Leu Val Gly Ser Val Gly Asp Leu Glu
35 40 45

Lys Thr Lys Met Thr Thr Leu Lys Lys Lys Asn Lys Met Trp Phe Trp
50 55 60

Asn Lys Ile Ser Ser Ser Gly Leu Lys Ile Pro Ser Phe Ser Tyr Gln
65 70 75 80

Phe Leu Gly Ser Val Lys Phe Asn Lys Ala Trp Trp Arg Lys Leu Val
85 90 95

Val Val Trp Val Val Phe Trp Val Leu Val Ser Ile Trp Thr Phe Trp
100 105 110

Tyr Phe Ser Ser Gln Ala Met Glu Lys Arg Lys Glu Thr Leu Ala Ser
115 120 125

Met Cys Asp Glu Arg Ala Arg Met Leu Gln Asp Gln Phe Asn Val Ser

130 135 140

Met Asn His Val Gln Ala Met Ser Ile Leu Ile Ser Thr Phe His His

145 150 155 160

Gly Lys Ile Pro Ser Ala Ile Asp Gln Arg Thr Phe Ser Glu Tyr Thr

165 170 175

Asp Arg Thr Ser Phe Glu Arg Pro Leu Thr Ser Gly Val Ala Tyr Ala

180 185 190

Met Arg Val Leu His Ser Glu Arg Glu Glu Phe Glu Arg Gln Gln Gly

195 200 205

Trp Thr Ile Arg Lys Met Tyr Ser Leu Glu Gln Asn Pro Val His Lys

210 215 220

Asp Asp Tyr Asp Leu Glu Ala Leu Glu Pro Ser Pro Val Gln Glu Glu

225 230 235 240

Tyr Ala Pro Val Ile Phe Ala Gln Asp Thr Val Ser His Val Val Ser

245 250 255

Leu Asp Met Leu Ser Gly Lys Glu Asp Arg Glu Asn Val Leu Arg Ala

260 265 270

Arg Ser Ser Gly Lys Gly Val Leu Thr Ala Pro Phe Pro Leu Ile Lys

275 280 285

Thr Asn Arg Leu Gly Val Ile Leu Thr Phe Ala Val Tyr Lys Arg Asp

290 295 300

Leu Pro Ser Asn Ala Thr Pro Lys Glu Arg Ile Glu Ala Thr Asn Gly

305 310 315 320

Tyr Leu Gly Gly Val Phe Asp Ile Glu Ser Leu Val Glu Asn Leu Leu

325 330 335

Gln Gln Leu Ala Ser Lys Gln Thr Ile Leu Val Asn Val Tyr Asp Ile

340 345 350

Thr Asn His Ser Gln Pro Ile Ser Met Tyr Gly Thr Asn Val Ser Ala

355 360 365

Asp Gly Leu Glu Arg Val Ser Pro Leu Ile Phe Gly Asp Pro Leu Arg

370 375 380

Lys His Glu Met Arg Cys Arg Phe Lys Gln Lys Pro Pro Trp Pro Val

385 390 395 400

Leu Ser Met Val Thr Ser Phe Gly Ile Leu Val Ile Ala Leu Leu Val

405 410 415

Ala His Ile Ile His Ala Thr Val Ser Arg Ile His Lys Val Glu Glu

420 425 430

Asp Cys Asp Lys Met Lys Gln Leu Lys Lys Lys Ala Glu Ala Ala Asp

435 440 445

Val Ala Lys Ser Gln Phe Leu Ala Thr Val Ser His Glu Ile Arg Thr

450 455 460

Pro Met Asn Gly Val Leu Gly Met Leu His Met Leu Met Asp Thr Glu

465 470 475 480

Leu Asp Val Thr Gln Gln Asp Tyr Val Arg Thr Ala Gln Ala Ser Gly

485 490 495

Lys Ala Leu Val Ser Leu Ile Asn Glu Val Leu Asp Gln Ala Lys Ile

500 505 510

Glu Ser Gly Lys Leu Glu Leu Glu Glu Val Arg Phe Asp Leu Arg Gly

515 520 525

Ile Leu Asp Asp Val Leu Ser Leu Phe Ser Ser Lys Ser Gln Gln Lys

530 535 540

Gly Val Glu Leu Ala Val Tyr Ile Ser Asp Arg Val Pro Asp Met Leu

545 550 555 560

Ile Gly Asp Pro Gly Arg Phe Arg Gln Ile Leu Thr Asn Leu Met Gly

565 570 575

Asn Ser Ile Lys Phe Thr Glu Lys Gly His Ile Phe Val Thr Val His

580 585 590

Leu Val Asp Glu Leu Phe Glu Ser Ile Asp Gly Glu Thr Ala Ser Ser

595 600 605

Pro Glu Ser Thr Leu Ser Gly Leu Pro Val Ala Asp Arg Gln Arg Ser

610 615 620

Trp Glu Asn Phe Lys Ala Phe Ser Ser Asn Gly His Arg Ser Phe Glu

625 630 635 640

Pro Ser Pro Pro Asp Ile Asn Leu Ile Val Ser Val Glu Asp Thr Gly

645 650 655

Val Gly Ile Pro Val Glu Ala Gln Ser Arg Ile Phe Thr Pro Phe Met

660 665 670

Gln Val Gly Pro Ser Ile Ser Arg Thr His Gly Gly Thr Gly Ile Gly

675 680 685

Leu Ser Ile Ser Lys Cys Leu Val Gly Leu Met Lys Gly Glu Ile Gly

690 695 700

Phe Ser Ser Thr Pro Lys Val Gly Ser Thr Phe Thr Phe Thr Ala Val

705 710 715 720

Phe Ser Asn Gly Met Gln Pro Ala Glu Arg Lys Asn Asp Asn Asn Gln

725 730 735

Pro Ile Phe Ser Glu Phe Arg Gly Met Lys Ala Val Val Val Asp His

740 745 750

Arg Pro Ala Arg Ala Lys Val Ser Trp Tyr His Phe Gln Arg Leu Gly

755 760 765

Ile Arg Val Glu Val Val Pro Arg Val Glu Gln Ala Leu His Tyr Leu

770 775 780

Lys Ile Gly Thr Thr Thr Val Asn Met Ile Leu Ile Glu Gln Glu Ile

785 790 795 800

Trp Asn Arg Glu Ala Asp Asp Phe Ile Lys Lys Leu Gln Lys Asp Pro

805 810 815

Leu Phe Leu Ser Pro Lys Leu Ile Leu Leu Ala Asn Ser Val Glu Ser

820 825 830

Ser Ile Ser Glu Ala Leu Cys Thr Gly Ile Asp Pro Pro Ile Val Ile

835 840 845

Val Lys Pro Leu Arg Ala Ser Met Leu Ala Ala Thr Leu Gln Arg Gly

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865 870 875 880

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885 890 895

Asp Asn Asn Val Asn Leu Arg Val Ala Ala Gly Ala Leu Lys Lys Tyr

900 905 910

Gly Ala Asp Val Val Cys Ala Glu Ser Gly Ile Lys Ala Ile Ser Leu

915 920 925

Leu Lys Pro Pro His Glu Phe Asp Ala Cys Phe Met Asp Ile Gln Met

930 935 940

Pro Glu Met Asp Gly Phe Glu Ala Thr Arg Arg Ile Arg Asp Met Glu

945 950 955 960

Glu Glu Met Asn Lys Arg Ile Lys Asn Gly Glu Ala Leu Ile Val Glu

965 970 975

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Asp Val Ile Gln Ala Thr His Glu Glu Cys Leu Lys Cys Gly Met Asp

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aga att gaa att tct gat tcc gag tca cta gaa aac ttg aaa agc agc 96

Arg Ile Glu Ile Ser Asp Ser Glu Ser Leu Glu Asn Leu Lys Ser Ser
20 25 30

gat ttt tat caa ctg ggt ggt ggt ggt gct ctg aat tcg tca gaa aag 144

Asp Phe Tyr Gln Leu Gly Gly Gly Gly Ala Leu Asn Ser Ser Glu Lys
35 40 45

ccg aga aag atc gat ttt tgg cgt tcg ggg ttg atg ggt ttt gcg aag 192

Pro Arg Lys Ile Asp Phe Trp Arg Ser Gly Leu Met Gly Phe Ala Lys
50 55 60

atg cag cag cag caa cag ctt cag cat tca gtg gcg gtg aag atg aac 240

Met Gln Gln Gln Gln Gln Leu Gln His Ser Val Ala Val Lys Met Asn
65 70 75 80

aat aat aat aat aac gat cta atg ggt aat aaa aaa ggg tca act ttc 288

Asn Asn Asn Asn Asn Asp Leu Met Gly Asn Lys Lys Gly Ser Thr Phe
85 90 95

ata caa gaa cat cga gca ttg tta cca aaa gct ttg att ctg tgg atc 336

Ile Gln Glu His Arg Ala Leu Leu Pro Lys Ala Leu Ile Leu Trp Ile
100 105 110

atc att gtt ggg ttt ata agc agt ggg att tat cag tgg atg gat gat 384

Ile Ile Val Gly Phe Ile Ser Ser Gly Ile Tyr Gln Trp Met Asp Asp
115 120 125

gct aat aag att aga agg gaa gag gtt ttg gtc agc atg tgt gat caa 432

Ala Asn Lys Ile Arg Arg Glu Glu Val Leu Val Ser Met Cys Asp Gln
130 135 140

aga gct aga atg ttg cag gat caa ttt agt gtt agt gtt aat cat gtt 480

Arg Ala Arg Met Leu Gln Asp Gln Phe Ser Val Ser Val Asn His Val
145 150 155 160

cat gct ttg gct att ctc gtc tcc act ttt cat tac cac aag aac cct 528

His Ala Leu Ala Ile Leu Val Ser Thr Phe His Tyr His Lys Asn Pro
165 170 175

tct gca att gat cag gag aca ttt gcg gag tac acg gca aga aca gca 576

Ser Ala Ile Asp Gln Glu Thr Phe Ala Glu Tyr Thr Ala Arg Thr Ala
180 185 190

ttt gag aga ccg ttg cta agt gga gtg gct tat gct gaa aaa gtt gtg 624

Phe Glu Arg Pro Leu Leu Ser Gly Val Ala Tyr Ala Glu Lys Val Val
195 200 205

aat ttt gag agg gag atg ttt gag cgg cag cac aat tgg gtt ata aag 672

Asn Phe Glu Arg Glu Met Phe Glu Arg Gln His Asn Trp Val Ile Lys
210 215 220

aca atg gat aga gga gag cct tca ccg gtt agg gat gag tat gct cct 720

Thr Met Asp Arg Gly Glu Pro Ser Pro Val Arg Asp Glu Tyr Ala Pro
225 230 235 240

gtt ata ttc tct caa gat agt gtc tct tac ctt gag tca ctc gat atg 768

Val Ile Phe Ser Gln Asp Ser Val Ser Tyr Leu Glu Ser Leu Asp Met
245 250 255

atg tca ggc gag gag gat cgt gag aat att ttg cga gct aga gaa acc 816

Met Ser Gly Glu Glu Asp Arg Glu Asn Ile Leu Arg Ala Arg Glu Thr
260 265 270

gga aaa gct gtc ttg act agc cct ttt agg ttg ttg gaa act cac cat 864

Gly Lys Ala Val Leu Thr Ser Pro Phe Arg Leu Leu Glu Thr His His
275 280 285

ctc gga gtt gtg ttg aca ttc cct gtc tac aag tct tct ctt cct gaa 912

Leu Gly Val Val Leu Thr Phe Pro Val Tyr Lys Ser Ser Leu Pro Glu
290 295 300

aat ccg act gtc gaa gag cgt att gca gcc act gca ggg tac ctt ggt 960

Asn Pro Thr Val Glu Glu Arg Ile Ala Ala Thr Ala Gly Tyr Leu Gly
305 310 315 320

ggt gcg ttt gat gtg gag tct cta gtc gag aat tta ctt ggt cag ctt 1008

Gly Ala Phe Asp Val Glu Ser Leu Val Glu Asn Leu Leu Gly Gln Leu
325 330 335

gct ggt aac caa gca ata gtt gtg cat gtg tat gat atc acc aat gca 1056

Ala Gly Asn Gln Ala Ile Val Val His Val Tyr Asp Ile Thr Asn Ala

340 345 350

tca gat cca ctt gtc atg tat ggt aat caa gat gaa gaa gcc gac aga 1104

Ser Asp Pro Leu Val Met Tyr Gly Asn Gln Asp Glu Glu Ala Asp Arg
355 360 365

tct ctc tct cat gag agc aag ctc gat ttt gga gac ccc ttc agg aaa 1152

Ser Leu Ser His Glu Ser Lys Leu Asp Phe Gly Asp Pro Phe Arg Lys
370 375 380

cat aag atg ata tgc agg tac cac caa aag gca cca ata cca ttg aat 1200

His Lys Met Ile Cys Arg Tyr His Gln Lys Ala Pro Ile Pro Leu Asn
385 390 395 400

gtg ctc aca act gtg cca ttg ttc ttt gcg att ggt ttc ttg gtg ggt 1248

Val Leu Thr Thr Val Pro Leu Phe Phe Ala Ile Gly Phe Leu Val Gly
405 410 415

tat ata ctg tat ggt gca gct atg cac ata gta aaa gtc gaa gat gat 1296

Tyr Ile Leu Tyr Gly Ala Ala Met His Ile Val Lys Val Glu Asp Asp
420 425 430

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Phe His Glu Met Gln Glu Leu Lys Val Arg Ala Glu Ala Ala Asp Val
435 440 445

gct aaa tcg cag ttt ctt gct acc gtg tct cac gag atc agg aca cca 1392

Ala Lys Ser Gln Phe Leu Ala Thr Val Ser His Glu Ile Arg Thr Pro
450 455 460

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Met Asn Gly Ile Leu Gly Met Leu Ala Met Leu Leu Asp Thr Glu Leu
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agc tcg aca cag aga gat tac gct caa acc gct caa gta tgt ggt aaa 1488

Ser Ser Thr Gln Arg Asp Tyr Ala Gln Thr Ala Gln Val Cys Gly Lys
485 490 495

gct ttg att gca ttg ata aat gag gtt ctt gat cgc gcc aag att gaa 1536

Ala Leu Ile Ala Leu Ile Asn Glu Val Leu Asp Arg Ala Lys Ile Glu
500 505 510

gct gga aag ctg gag ttg gaa tca gta cca ttt gat atc cgt tca ata 1584

Ala Gly Lys Leu Glu Leu Glu Ser Val Pro Phe Asp Ile Arg Ser Ile
515 520 525

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Leu Asp Asp Val Leu Ser Leu Phe Ser Glu Glu Ser Arg Asn Lys Gly
530 535 540

att gag ctc gcg gtt ttc gtt tca gac aaa gta cca gag ata gtc aaa 1680

Ile Glu Leu Ala Val Phe Val Ser Asp Lys Val Pro Glu Ile Val Lys
545 550 555 560

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Gly Asp Ser Gly Arg Phe Arg Gln Ile Ile Ile Asn Leu Val Gly Asn
565 570 575

tcg gtt aaa ttc aca gag aaa gga cat atc ttt gtt aaa gtc cat ctt 1776

Ser Val Lys Phe Thr Glu Lys Gly His Ile Phe Val Lys Val His Leu
580 585 590

gcg gaa caa tca aaa gat gaa tct gaa ccg aaa aat gca ttg aat ggt 1824

Ala Glu Gln Ser Lys Asp Glu Ser Glu Pro Lys Asn Ala Leu Asn Gly
595 600 605

gga gtg tct gaa gaa atg atc gtt gtt tcc aaa cag tca agt tac aac 1872

Gly Val Ser Glu Glu Met Ile Val Val Ser Lys Gln Ser Ser Tyr Asn
610 615 620

aca ttg agc ggt tac gaa gct gct gat ggt cgg aat agc tgg gat tca 1920

Thr Leu Ser Gly Tyr Glu Ala Ala Asp Gly Arg Asn Ser Trp Asp Ser
625 630 635 640

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Phe Lys His Leu Val Ser Glu Glu Gln Ser Leu Ser Glu Phe Asp Ile
645 650 655

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660 665 670

atc cct tta gtt gca caa ggc cgt gtg ttt atg ccg ttt atg caa gca 2064

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675 680 685

gat agc tcg act tca aga aac tat gga ggt act ggt att ggt ttg agt 2112

Asp Ser Ser Thr Ser Arg Asn Tyr Gly Gly Thr Gly Ile Gly Leu Ser
690 695 700

ata agc aag tgt ctt gtt gaa ctt atg cgt ggt cag ata aat ttc ata 2160

Ile Ser Lys Cys Leu Val Glu Leu Met Arg Gly Gln Ile Asn Phe Ile
705 710 715 720

agc cgg cct cat att gga agc acg ttc tgg ttc acg gct gtt tta gag 2208

Ser Arg Pro His Ile Gly Ser Thr Phe Trp Phe Thr Ala Val Leu Glu
725 730 735

aaa tgc gat aaa tgc agt gcg att aac cat atg aag aaa cct aat gtg 2256

Lys Cys Asp Lys Cys Ser Ala Ile Asn His Met Lys Lys Pro Asn Val
740 745 750

gaa cac ttg cct tct act ttt aaa gga atg aaa gct ata gtt gtt gat 2304

Glu His Leu Pro Ser Thr Phe Lys Gly Met Lys Ala Ile Val Val Asp

755 760 765

gct aag cct gtt aga gct gct gtg act aga tac cat atg aaa aga ctc 2352

Ala Lys Pro Val Arg Ala Ala Val Thr Arg Tyr His Met Lys Arg Leu
770 775 780

gga atc aat gtt gat gtc gtg aca agt ctc aaa acc gct gtt gtt gca 2400

Gly Ile Asn Val Asp Val Val Thr Ser Leu Lys Thr Ala Val Val Ala
785 790 795 800

gct gct gcg ttt gaa aga aac ggt tct cct ctc cca aca aaa ccg caa 2448

Ala Ala Ala Phe Glu Arg Asn Gly Ser Pro Leu Pro Thr Lys Pro Gln
805 810 815

ctt gat atg atc tta gta gag aaa gat tca tgg att tca act gaa gat 2496

Leu Asp Met Ile Leu Val Glu Lys Asp Ser Trp Ile Ser Thr Glu Asp
820 825 830

aat gac tca gag att cgt tta ttg aat tca aga acc aac gga aac gtt 2544

Asn Asp Ser Glu Ile Arg Leu Leu Asn Ser Arg Thr Asn Gly Asn Val
835 840 845

cat cac aag tct ccg aaa cta gct cta ttc gca aca aac atc aca aat 2592

His His Lys Ser Pro Lys Leu Ala Leu Phe Ala Thr Asn Ile Thr Asn
850 855 860

tcg gag ttc gac aga gct aaa tcc gca gga ttt gca gat acg gta ata 2640

Ser Glu Phe Asp Arg Ala Lys Ser Ala Gly Phe Ala Asp Thr Val Ile
865 870 875 880

atg aaa ccg tta aga gca agc atg att ggg gcg tgt ctg caa caa gtt 2688

Met Lys Pro Leu Arg Ala Ser Met Ile Gly Ala Cys Leu Gln Gln Val
885 890 895

ctc gag ctg aga aaa aca aga caa caa cat cca gaa gga tca tca ccc 2736

Leu Glu Leu Arg Lys Thr Arg Gln Gln His Pro Glu Gly Ser Ser Pro
900 905 910

gca act ctc aag agc ttg ctt aca ggg aag aag att ctt gtg gtt gat 2784

Ala Thr Leu Lys Ser Leu Leu Thr Gly Lys Lys Ile Leu Val Val Asp
915 920 925

gat aat ata gtt aac agg aga gta gct gca gga gct ctc aag aaa ttt 2832

Asp Asn Ile Val Asn Arg Arg Val Ala Ala Gly Ala Leu Lys Lys Phe
930 935 940

gga gca gaa gtg gtt tgt gca gag agt ggt caa gtt gct ttg ggt ttg 2880

Gly Ala Glu Val Val Cys Ala Glu Ser Gly Gln Val Ala Leu Gly Leu
945 950 955 960

ctt cag att cca cac act ttc gat gct tgc ttc atg gat att caa atg 2928

Leu Gln Ile Pro His Thr Phe Asp Ala Cys Phe Met Asp Ile Gln Met
965 970 975

cca cag atg gac gga ttt gaa gca act cgt cag ata aga atg atg gag 2976

Pro Gln Met Asp Gly Phe Glu Ala Thr Arg Gln Ile Arg Met Met Glu
980 985 990

aag gaa gct aaa gag aag acg aat ctc gaa tgg cat tta ccg att cta 3024

Lys Glu Ala Lys Glu Lys Thr Asn Leu Glu Trp His Leu Pro Ile Leu
995 1000 1005

gcg atg act gcg gat gtg ata cac gcg acc tac gag gaa tgt ctg aaa 3072

Ala Met Thr Ala Asp Val Ile His Ala Thr Tyr Glu Glu Cys Leu Lys
1010 1015 1020

agt ggg atg gat ggt tac gtc tcc aaa cct ttt gaa gaa gag aat ctc 3120

Ser Gly Met Asp Gly Tyr Val Ser Lys Pro Phe Glu Glu Glu Asn Leu
1025 1030 1035 1040

tat aaa tcc gtt gcc aaa tca ttc aaa cct aat cct atc tca cct tcg 3168

Tyr Lys Ser Val Ala Lys Ser Phe Lys Pro Asn Pro Ile Ser Pro Ser
1045 1050 1055

tcg taa 3174

Ser

<210> 6
<211> 1057
<212> PRT
<213> Arabidopsis thaliana

<400> 6
Met Asn Trp Ala Leu Asn Asn His Gln Glu Glu Glu Glu Glu Pro Arg

1 5 10 15

Arg Ile Glu Ile Ser Asp Ser Glu Ser Leu Glu Asn Leu Lys Ser Ser

20 25 30

Asp Phe Tyr Gln Leu Gly Gly Gly Gly Ala Leu Asn Ser Ser Glu Lys

35 40 45

Pro Arg Lys Ile Asp Phe Trp Arg Ser Gly Leu Met Gly Phe Ala Lys

50 55 60

Met Gln Gln Gln Gln Gln Leu Gln His Ser Val Ala Val Lys Met Asn

65 70 75 80

Asn Asn Asn Asn Asn Asp Leu Met Gly Asn Lys Lys Gly Ser Thr Phe

85 90 95

Ile Gln Glu His Arg Ala Leu Leu Pro Lys Ala Leu Ile Leu Trp Ile

100 105 110

Ile Ile Val Gly Phe Ile Ser Ser Gly Ile Tyr Gln Trp Met Asp Asp

115 120 125

Ala Asn Lys Ile Arg Arg Glu Glu Val Leu Val Ser Met Cys Asp Gln

130 135 140

Arg Ala Arg Met Leu Gln Asp Gln Phe Ser Val Ser Val Asn His Val

145 150 155 160

His Ala Leu Ala Ile Leu Val Ser Thr Phe His Tyr His Lys Asn Pro

165 170 175

Ser Ala Ile Asp Gln Glu Thr Phe Ala Glu Tyr Thr Ala Arg Thr Ala

180 185 190

Phe Glu Arg Pro Leu Leu Ser Gly Val Ala Tyr Ala Glu Lys Val Val

195 200 205

Asn Phe Glu Arg Glu Met Phe Glu Arg Gln His Asn Trp Val Ile Lys

210 215 220

Thr Met Asp Arg Gly Glu Pro Ser Pro Val Arg Asp Glu Tyr Ala Pro
225 230 235 240

Val Ile Phe Ser Gln Asp Ser Val Ser Tyr Leu Glu Ser Leu Asp Met
245 250 255

Met Ser Gly Glu Glu Asp Arg Glu Asn Ile Leu Arg Ala Arg Glu Thr
260 265 270

Gly Lys Ala Val Leu Thr Ser Pro Phe Arg Leu Leu Glu Thr His His
275 280 285

Leu Gly Val Val Leu Thr Phe Pro Val Tyr Lys Ser Ser Leu Pro Glu
290 295 300

Asn Pro Thr Val Glu Glu Arg Ile Ala Ala Thr Ala Gly Tyr Leu Gly
305 310 315 320

Gly Ala Phe Asp Val Glu Ser Leu Val Glu Asn Leu Leu Gly Gln Leu
325 330 335

Ala Gly Asn Gln Ala Ile Val Val His Val Tyr Asp Ile Thr Asn Ala
340 345 350

Ser Asp Pro Leu Val Met Tyr Gly Asn Gln Asp Glu Glu Ala Asp Arg
355 360 365

Ser Leu Ser His Glu Ser Lys Leu Asp Phe Gly Asp Pro Phe Arg Lys
370 375 380

His Lys Met Ile Cys Arg Tyr His Gln Lys Ala Pro Ile Pro Leu Asn
385 390 395 400

Val Leu Thr Thr Val Pro Leu Phe Phe Ala Ile Gly Phe Leu Val Gly
405 410 415

Tyr Ile Leu Tyr Gly Ala Ala Met His Ile Val Lys Val Glu Asp Asp

420 425 430

Phe His Glu Met Gln Glu Leu Lys Val Arg Ala Glu Ala Ala Asp Val

435 440 445

Ala Lys Ser Gln Phe Leu Ala Thr Val Ser His Glu Ile Arg Thr Pro

450 455 460

Met Asn Gly Ile Leu Gly Met Leu Ala Met Leu Leu Asp Thr Glu Leu

465 470 475 480

Ser Ser Thr Gln Arg Asp Tyr Ala Gln Thr Ala Gln Val Cys Gly Lys

485 490 495

Ala Leu Ile Ala Leu Ile Asn Glu Val Leu Asp Arg Ala Lys Ile Glu

500 505 510

Ala Gly Lys Leu Glu Leu Glu Ser Val Pro Phe Asp Ile Arg Ser Ile

515 520 525

Leu Asp Asp Val Leu Ser Leu Phe Ser Glu Glu Ser Arg Asn Lys Gly

530 535 540

Ile Glu Leu Ala Val Phe Val Ser Asp Lys Val Pro Glu Ile Val Lys

545 550 555 560

Gly Asp Ser Gly Arg Phe Arg Gln Ile Ile Ile Asn Leu Val Gly Asn

565 570 575

Ser Val Lys Phe Thr Glu Lys Gly His Ile Phe Val Lys Val His Leu

580 585 590

Ala Glu Gln Ser Lys Asp Glu Ser Glu Pro Lys Asn Ala Leu Asn Gly

595 600 605

Gly Val Ser Glu Glu Met Ile Val Val Ser Lys Gln Ser Ser Tyr Asn

610 615 620

Thr Leu Ser Gly Tyr Glu Ala Ala Asp Gly Arg Asn Ser Trp Asp Ser

625 630 635 640

Phe Lys His Leu Val Ser Glu Glu Gln Ser Leu Ser Glu Phe Asp Ile

645 650 655

Ser Ser Asn Val Arg Leu Met Val Ser Ile Glu Asp Thr Gly Ile Gly

660 665 670

Ile Pro Leu Val Ala Gln Gly Arg Val Phe Met Pro Phe Met Gln Ala

675 680 685

Asp Ser Ser Thr Ser Arg Asn Tyr Gly Gly Thr Gly Ile Gly Leu Ser

690 695 700

Ile Ser Lys Cys Leu Val Glu Leu Met Arg Gly Gln Ile Asn Phe Ile

705 710 715 720

Ser Arg Pro His Ile Gly Ser Thr Phe Trp Phe Thr Ala Val Leu Glu

725 730 735

Lys Cys Asp Lys Cys Ser Ala Ile Asn His Met Lys Lys Pro Asn Val

740 745 750

Glu His Leu Pro Ser Thr Phe Lys Gly Met Lys Ala Ile Val Val Asp

755 760 765

Ala Lys Pro Val Arg Ala Ala Val Thr Arg Tyr His Met Lys Arg Leu

770 775 780

Gly Ile Asn Val Asp Val Val Thr Ser Leu Lys Thr Ala Val Val Ala

785 790 795 800

Ala Ala Ala Phe Glu Arg Asn Gly Ser Pro Leu Pro Thr Lys Pro Gln

805 810 815

Leu Asp Met Ile Leu Val Glu Lys Asp Ser Trp Ile Ser Thr Glu Asp

820 825 830

Asn Asp Ser Glu Ile Arg Leu Leu Asn Ser Arg Thr Asn Gly Asn Val

835 840 845

His His Lys Ser Pro Lys Leu Ala Leu Phe Ala Thr Asn Ile Thr Asn

850 855 860

Ser Glu Phe Asp Arg Ala Lys Ser Ala Gly Phe Ala Asp Thr Val Ile

865 870 875 880

Met Lys Pro Leu Arg Ala Ser Met Ile Gly Ala Cys Leu Gln Gln Val

885 890 895

Leu Glu Leu Arg Lys Thr Arg Gln Gln His Pro Glu Gly Ser Ser Pro

900 905 910

Ala Thr Leu Lys Ser Leu Leu Thr Gly Lys Lys Ile Leu Val Val Asp

915 920 925

Asp Asn Ile Val Asn Arg Arg Val Ala Ala Gly Ala Leu Lys Lys Phe

930 935 940

Gly Ala Glu Val Val Cys Ala Glu Ser Gly Gln Val Ala Leu Gly Leu

945 950 955 960

Leu Gln Ile Pro His Thr Phe Asp Ala Cys Phe Met Asp Ile Gln Met

965 970 975

Pro Gln Met Asp Gly Phe Glu Ala Thr Arg Gln Ile Arg Met Met Glu

980 985 990

Lys Glu Ala Lys Glu Lys Thr Asn Leu Glu Trp His Leu Pro Ile Leu

995 1000 1005

Ala Met Thr Ala Asp Val Ile His Ala Thr Tyr Glu Glu Cys Leu Lys

1010 1015 1020

Ser Gly Met Asp Gly Tyr Val Ser Lys Pro Phe Glu Glu Glu Asn Leu

1025 1030 1035 1040

Tyr Lys Ser Val Ala Lys Ser Phe Lys Pro Asn Pro Ile Ser Pro Ser

1045 1050 1055

Ser

<210> 7

<211> 125

<212> PRT

<213> Saccharomyces cerevisiae

<400> 7

Glu Thr Ser Val Lys Ile Leu Val Val Glu Asp Asn His Val Asn Gln
1 5 10 15

Glu Val Ile Lys Arg Met Leu Asn Leu Glu Gly Ile Glu Asn Ile Glu
20 25 30

Leu Ala Cys Asp Gly Gln Glu Ala Phe Asp Lys Val Lys Glu Leu Thr
35 40 45

Ser Lys Gly Glu Asn Tyr Asn Met Ile Phe Met Asp Val Gln Met Pro
50 55 60

Lys Val Asp Gly Leu Leu Ser Thr Lys Met Ile Arg Arg Asp Leu Gly
65 70 75 80

Tyr Thr Ser Pro Ile Val Ala Leu Thr Ala Phe Ala Asp Asp Ser Asn
85 90 95

Ile Lys Glu Cys Leu Glu Ser Gly Met Asn Gly Phe Leu Ser Lys Pro
100 105 110

Ile Lys Arg Pro Lys Leu Lys Thr Ile Leu Thr Glu Phe
115 120 125

<210> 8
<211> 118
<212> PRT
<213> Escherichia coli

<400> 1
Asn Asp Asp Met Met Ile Leu Val Val Asp Asp His Pro Ile Asn Arg
1 5 10 15

Arg Leu Leu Ala Asp Gln Leu Gly Ser Leu Gly Tyr Gln Cys Lys Thr
20 25 30

Ala Asn Asp Gly Val Asp Ala Leu Asn Val Leu Ser Lys Asn His Ile
35 40 45

Asp Ile Val Leu Ser Asp Val Asn Met Pro Asn Met Asp Gly Tyr Arg

50 55 60

Leu Thr Gln Arg Ile Arg Gln Leu Gly Leu Thr Leu Pro Val Ile Gly
65 70 75 80

Val Thr Ala Asn Ala Leu Ala Glu Glu Lys Gln Arg Cys Leu Glu Ser
85 90 95

Gly Met Asp Ser Cys Leu Ser Lys Pro Val Thr Leu Asp Val Ile Lys
100 105 110

Gln Ser Leu Thr Leu Tyr
115

<210> 9
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 9
tccccgcgga aaatgttctt acggttaggt ag 32

<210> 10

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed oligonucleotide primer for PCR

<400> 10

tcggtcgact tatgattctg tatctgaagg cga 33

<210> 11

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed oligonucleotide primer for PCR

<400> 11

tcagatatga actgggcact caac 24

<210> 12

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 12

ctcaatgctt ttgttccttg actc 24

<210> 13

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed

oligonucleotide primer for PCR

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accatgaact gggcactcaa caatcatcaa g 31

<210> 14

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 14

ggattacgac gaaggtgaga taggattagg 30

<210> 15

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed oligonucleotide primer for PCR

<400> 15

gatcccagct agctagggcc ctaccgcggg ga 32

<210> 16

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed oligonucleotide primer for PCR

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tccccgcgga aaatgttctt acggttaggt ag 32

<210> 17

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 17

tcggtcgact tatgattctg tatctgaagg cga 33

<210> 18

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 18

ctagtccccg cggtagggcc ctagctagct gg 32

<210> 19

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed oligonucleotide primer for PCR

<400> 19

tccccgcgga aaatgtctat aacttgtgag c 31

<210> 20

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed oligonucleotide primer for PCR

<400> 20

ctagctagct taacaaggtt caaagaatct tgc 33

<210> 21

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed oligonucleotide primer for PCR

<400> 21

tccccgcgga aaatgaaagc acgaggtgag agg 33

<210> 22

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed oligonucleotide primer for PCR

<400> 22

ctagctagct taacaaggtt caaagaattt gc 32